Amendment

In the specification:

1.   Page 11, replace first full paragraph (lines 6 through 20):

--/ Figure 15 shows the Soybean hydrophobic protein (HP) cDNA and deduced amino acid sequences. Figure 15(a), the cDNA and amino acid sequence of HP (SEQ ID NO:10). The pre-protein signal sequence is underlines. Figure 15(b) shows the deduced amino acid sequence of HP pre-protein. Alternate *N*-terminal residues are boxed, as determined by peptide microsequence analysis. Figure 15(c) shows a Kyle-Doolittle hydrophilicity plot of HP (Lasergene). In this plot, positive values indicate greater hydrophilic character. Also represented are the three domains of the HP pre-protein and the length of the mature peptide. Figure 15(d) shows a schematic comparison of HP domain structure to three other plant proteins. Bold numbers indicate the length in amino acid residues for the domain segments. The pattern of spacing between the eight cysteine residues within the hydrophobic domains is also shown below each protein. Sequences for tobacco N16 polypeptide (D86629), maize proline rich hydrophobic protein (PRHP) (X60432), and *Arabidopsis* lipid transfer protein 1 (LTP1) (M80567) were retrieved from GenBank --

2.   Page 12, replace second full paragraph (lines 16 through 30):

--| Figure 19 shows the nucleotide sequence and deduced amino acid sequence of SC4 cDNA (SEQ ID NO:11), and the sequence comparisons between SC4 protein and BURP proteins. Figure 19(s), 5' and 3' untranslated sequences are in lowercase lettering. The stop codon is shown with an asterisk and two polyadenylation signals are underlined. Two copies of a ten amino acid repeat is also underlined. Concensus sequences for *N*-glycosylation (NNT; NSSN; and NGTV) are also underlined. Figure 19(b), amino acid alignment of the carboxyl terminus of the SC4 protein with the BURP domain (A) and the amino terminus of the SC4 protein with the conserved segments of the second domain (B) of several BURP domain

proteins. Pg1β is not included in panel B as the second domain of this protein does not contain a conserved segment. Gaps were introduced to optimize the alignment. Conserved amino acids are shown in bold face. Amino aids of each protease are numbered from the precursor sequence. Figure 19(c) shows the structural similarity between SC4 protein and the BURP domain proteins.

3.   Page 13, replace paragraph bridging to page 14:

-- Figure 23 reveals the characterization of *sc*20 and SC20 protein. Figure 23(a) is a restriction map of *sc*20. Figure 23(b) shows the nucleotide sequence and deduced amino acid sequence of *sc*20 cDNA (SEQ ID NO:12). The stop codon is shown with an asterisk and the polyadenylation signal is underlined. The concensus sequences for *N*-glycosylation are also underlined. Figure 23(c) shows the hydrophobic plot of SC20 protein, where hydrophobic regions possess a positive sign, and hydrophilic regions possess a negative sign. In Figure 23(d), alignment of SC20 protein with other subtilases is shown. D, H and S regions represent amino acid sequences around the catalytic aspartate, histidine and serine residues of the subtilases. The catalytic residues are labeled with an asterisk. *N* region represents amino acid sequence around the conserved asparagine residue, of subtilases. # indicates the conserved asparagine. AF70, cucumisin, P69B, Ag12, subtilisin BPN', kex2, furin are from *Picea abies, Cucumis melo* L., *Lycopersicon esculentum, Alnus glutinosa, Bacillus subtilis, Saccharomyces cerevisiae,* and *Homo sapiens* respectively. Conserved amino acids are shown in boldface. Amino acids of each protease are numbered from the precursor sequence. --

4.   Please cancel pages 1/33 through 33/33 of the parent PCT application (WO 99/53067), entitled "SEQUENCE LISTING", without prejudice.

5.   Insert the accompanying 44 pages, entitled "SEQUENCE LISTING", following the final paragraph of page 72 of the parent PCT application (WO 99/53067).